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tigr-gss-
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                                                                                                                                                                                                                                                                                                                           AQ874584.1 GI:6286828
AQ874584.1 GI:6286828
GSS.
Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;
                                                                                                                                                       Email: anuj.kumar@yale.edu
te of mTn-3xHA/lacZ Insertion.
Seq primer: GGCCTTCTTTCTTTGGAAGTAC
Class: transposon-tagged.
                                                                                                                                                                                        P.O. Box 208103, 1
Tel: 203 432 9949
Fax: 203 432 6161
                                                                                                                                                                                                                                               Gene Disruption Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                   AQ874584 1ine V111B3 mTn-3xHA/lacZ Insertion Library, strain Cerevisiae genomic 5', genomic survey sequence.
                                                                                                                                                                                                                                                                                                    1 (bases 1 to 434)
Ross-Macdonald, P., Roemer, T.,
                                                                                                                                                                                                                             Contact: Kumar
Michael Snyder,
                                                                                                                                                                                                                      Yale University
                                                                                                                                                                                                                                                                                                                       Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                             transposon-tagged.
Location/Qualifiers
                        /clone_lib="mTn-3xHA/lacZ Insertion Library, strain Y2278"
/note="Vector: pHSS6-Sa1; A yeast genomic DNA library
without 2 micron or mitochondrial DNA was prepared in
pHSS6-Sa1; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a mTn-3xHA/lacZ
minitransposon containing lacZ, URA3, and tet resistance.
                                                                                                                                                                                                                                     Kumar A
                                                                                      /organism="Saccharomyces cerevisiae"
/mol type="genomic DNA"
/strain="Y2278 - S288C background, c
/db xref="taxon:4932"
/lab host="E. coli"
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CE498419 Tegr-989-
CL510366 SAIL B29
AL064465 Drosophil
AW633159 bl04d09 x
AQ383493 RPCII1-15
CE806390 tigr-988-
AG435289 Mus museu
AW13335 se17e08.y
AG157962 Pan trogl
BZ312600 id27a07.9
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Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zyosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Bon,E., Neuveglise,C., Casaregola,S., Artiguenave,F., Aigle,M. and Durrens,P. Genomic exploration of the hemiascomycetous yeasts: 5. Saccharomyces bayanus var. uvarum FEBS Lett. 487 (1), 37-41 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNS06GVN 927 bp DNA linear GSS 30-NOV-2001 T3 end of clone AS0AA007G06 of library ASOAA from strain CLIB 533 of Saccharomyces bayanus, genomic survey sequence.
AL398217 AL398217.1 GI:12151528 GSS.
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1 (bases 1 to 927)
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                                                                                                                                                                                                                                  Drosophila melanogaster genome BACR19021 of RPCI-98 library f: fly), genomic survey sequence.
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.f:
- Web : www.genoscope.cns.fr)
                                                                                                                                                                                      GSS.
                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insu
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                   Drosophila melanogaster (fruit
Drosophila melanogaster
                                             Genoscope
Direct Submission
                                                                                                                                                                                                      AL052985.1
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AL052985
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strong similarity to YKR076w and YGR154c ]"
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/note="end : T3"
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/db_xref="taxon:4931"
/clone="ASOAA007G06"
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/strain="CLIB 533"
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Pred. No. 6.7e-29;
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Best Local :
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                                                                                                  genomic survey sequence.

NC252581.1 GI:30589331
GSS.
Gallus gallus (chicken)
SM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
E 1 (bases 1 to 1055)
SKremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
Warren, W., Graves, T., Mardis, E. and Wilson, R.
Gallus gallus BAC End Reads
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clomes, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                441 WTGAAATAAGAGTTTTTATGCTTCTKAAAWGCTGAAATACATWTTCKDWKKGKKGKCSGC
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CH261-136H21_Sp6.1 CH261 Gallus
             Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
                                                                                    Contact: Richard K. Wilson
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/db_xref="taxon:7227"
/clone="BACR19021"
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GSS.
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                                                                                                                                                                                                                                    Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Brdopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37F10 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Gallus gallus"
/mol_type="qenomic אום"
                    /clone_lib="DrosBAC"
/plasmīd="pBeloBAC11"
                                                                                    /mol_type="genomic DN
/db_xref="taxon:7227"
                                                                                                                             organism="Drosophila melanogaster'
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/clone_lib="CH261"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="female"
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/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                  Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster genome survey sequence SP6 end of BAC PACNO8K14 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL101624.1
GSS.
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                                            AATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCTTAACTTTTATTGCAGAGGACTAT 676
                                                                                                             AGCAAGCGGAAAAAACTATGGCTAGCTGGGAGTTGTTTTTCAATCATATAAAAGGGAGA 616
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              AACTATGGDTAAMTTTAWWAATTTTHTAAAGGGAAGAWTTWTTTTTTTAAGKGGCCTWT
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/plasmid="pBeloBAC11"
                                                                                                                                                                                                                                                                                                 /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                 clone="BACN08K14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: L. David Sibley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WashU Plasmodium EST Project
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                                                                      TTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTTCTGGGACGTC
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57.3%;
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Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
Library was constructed by R. Haywood. DNA sequencing by:
Library was constructed by R. Haywood. DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
Tel: 314 286 1800
Fax: 314 286 1810
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Plasmodium falciparum 3D7
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 436)
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                                                                                                                                                      /note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2: KhoI; The library was constructed by R Haywood. cDNAs were synthesized from ganetocyte poly(A)+ RNA by oligo d(T) priming, size-selected and directionally cloned into the EcoRi (5' end) to XhoI (3' end) sites of the Uni-ZAP XR lambda vector (Stratagene). The primary library was mass excised as phagemid using the Exassist helper phage (Stratagene). Clones were mass excised using the Exassist helper phage (Stratagene), the phagemid the Exassist helper phage (Stratagene), the phagemids were precitptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells. Clone
                                                                           Availability: David Sibley, Washington University."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="gametocyte (stage III-V)"
/lab_host="DH10B (GeneHog, Invitrogen,
/clone__ib="Plasmodium falciparum 3D7 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:36329"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (33-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr )

By 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr )

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN03G04 of DrosBAC library from Drosophila melanogaster (fruit
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/plasmīd="pBeloBAC11"
/note="end : SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
|mol_type="genomic DNA"
|/db_xref="taxon:7227"
|/clone="BACN03G04"
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BOGTD44TF BOGT Brassica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, J (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC Clones are derived from the mouse BAC library MSMg01.
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Sequences of Library MSMg01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue type="mixture of kidney and spleen"/clone_Tib="MSMg01 Mouse Male BAC Library"
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/sex="male"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mam
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs -r@mail.nih.gov
Tissue Procurement: ATCC
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Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSs: BOGTD44TR
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                    BI255759.1
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DNA is from a doubled haploid
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ilarity 50.0%;
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Library Preparation: Life Technologies, Library Arrayed by: Incyte Genomics, In
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/clone_lib="BOGT"
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/strain="TO1000DH3"
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High quality sequence stop: 711.
Location/Qualifiers
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db_xref="taxon:9606"
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AL214492.1 GI:7873311
GSS; genome survey sequence.
GSS; genome nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
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                                                                                                                                                                                                                                                                                Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11298 row: o column: 19
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."
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                                                                                                                       Dasilva,C., Ozouf.
u,L., Billault,A.,
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                                                                                                                                                                                                                                                      ESTs from a tomato flower library
Unpublished (2001)
Contact: Rutger S. van der Hoeven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web: www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                                                                                                               252 Emerson Hall, Ithaca, NY 14850, USA
Tel: 607 255 7886
Fax: 607 255 6683
                                                                                                                                                                                                                                         Contact: Rutger S. van der Hoeven Cornell University
                                                                                                                                                                                                                                                                                                  van der Hoeven, R.S. and Tanksley, S.D.
                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
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Lycopersicon
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Direct Submission
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ilarity 45.4%;
Conservative 1
                                                                                                                                                                                    rv19@cornell.edu
 developmental stages"
                                                                                               organism="Lycopersicon esculentum"
|mol_type="mRNA"
|cultivar="E6203"
              /tissue_type="developing flower buds
/dav_stage="4-8 week old plants"
/lab_host="XLOLR"
/clone_lib="Tomato flower library fro
                                                                                                                                                      Location/Qualifiers
                                                                     /db_xref="taxon:4081"
/clone="cC-esflcLEL23G13d1"
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/clone="167C22"
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Pred. No. 4.3;
L9; Mismatches
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16 AAAAAAAAAAAAAAA 1
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Unpublished (1997)
Contact: Takuji Sasaki
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
National Institute of Program, Kannondai 2-1-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 518)
Yamamoto, K. and Sasaki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AU077905.1 GI:5667645
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AU077905 Sice shoot Oryza sativa clone S5033 8z, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 81-298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 81-298-38-7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rice cDNA from etiolated shoot
                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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AAAAAGACTAATAATA 719
                                                                                                         TTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCTT
                                                                                                                                               5.5%;
nilarity 57.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         tsasaki@abr.affrc.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBK_CMV; Site_1: EcoRI; Site_2: XhoI;
Flowers and flower buds were collected from greenhouse
grown plants and used for library construction (cLEL)
                                                                                                                                                                                                                                            /dev_stage="ETiolated shoot (8 days ./clone_lib="Rice shoot"
/clone_Tib="Rice shoot"
/note="Etiolated shoot (8 days old)"
                                                                                                                                                                                                                                                                                                      /cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="S5033_8Z"
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                                                                                                                                                                                                                                                                                                                                                            organism="Oryza sativa/mol_type="mRNA"
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AUTHORS
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VERSION
KEYWORDS
SOURCE
Job time :
                    Search completed: August 27,
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AZ541311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MI
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba
                                                                                  527 TTATGAAAAATAATAT
                                                                                                                            708
                                                                                                                                                                                                                                                             407
                                                                                                                                                                                                                                                                                                                                              76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 845)

Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences
HM1: MSS sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence start: 42
High quality sequence stop: 612.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: M13-Reverse Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Entamoeba histolytica
Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic, genomic survey sequence. AZ541311
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                                                                                                                                                                                                                                                                                      AGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGG 647
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  secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G. and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="HM1:IMSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Entamoeba histolytica"
                                                                                                                                                                                                                                                                                                                                                               55.9%;
                    2005, 10:01:40
                                                                                    542
                                                                                                                                                                                                                                                                                                                                           0;
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Pred. No. 4.8;
0; Mismatches 6
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Result
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Maximum Match 10
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Perfect score:
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length: 2000000000
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Match
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723
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1: geneseqn1980s:*
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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ABS51325
ADT96256
AAS29224
ABA16123
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ADC25486
ABV04394
AAL35477
ABX58465
ADJ28192
ABX36811
ABQ59188
ADS41207
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AAD07493
AAD07503
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8060.213 Million cell updates/sec
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       Aad07475 Yeast pro
Aad07497 pYMR251Ap
Aad07493 Yeast YMR
Aad07503 Yeast YMR
Abd76446 S. cerevi
Ada71938 Rice gene
Abs51325 CDNA enco
Adt96256 COlon can
Aas29224 Genomic s
Aba16123 Human ner
Abs68364 Human CDN
Abv04394 Human pro
Aal35476 Human mus
Abx58465 CDNA enco
Ad13617 Human mus
Abx58465 CDNA enco
Ad13611 Bovine ES
Abg59188 Human col
Ad346110 Filman aut
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4.9 107	4.9	.9	4.9	4.9	4.9	٠,	4.9 33	4.9	4.9 64		.9	.9	.0	4.9		5.0		5.0	5.0	5.0			5.0	5.0 110
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ADQ97316	ADS89390	ACN88712	ADA71938	AAZ41383	ABV96856	ACA64924	AAK70003	ABV18166	ACN37231	ADI82483	ADH29006	ABK09744	ABL58962	ACH17729	ADS89438	ACA40062	ADA56114	ACC50510	ADA39926	AAZ00806	ACN62578	ABL34113	ABT22885	ADS36499
Adq97316 Mouse can	Ads89390 Oligonucl		Ada71938 Rice gene	Aaz41383 Human nor	Abv96856 Human pan	Aca64924 Human PL2	Aak70003 Human imm	Abv18166 Human pro	Acn37231 Human per	Adi82483 Human mod	Adh29006 Human chr	Abk09744 Human ova	Ab158962 Human tum	Ach17729 Human adu	Ads89438 Oligonucl	Aca40062 Prokaryot	Ada56114 Gene enco	Acc50510 Human sec	Ada39926 Human sec	Aaz00806 Human sec	Acn62578 Cotton de	Abl34113 Human imm	Abt22885 Breast ca	Ads36499 Human aut

## ALIGNMENTS

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RESULT 1
AAD07475
ID AAD0
XX AAD0
AC AAD0
XX Yeas
XX Yeas
XX Yeas
XX Yeas
XX Yeas
XX WO20
XX Sacc
XX WO20
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XX WO20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-NOV-1999;
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The invention relates to yeast promoters that are used to control the expression of homologous and heterologous nucleic acids encoding proteins and polypeptides in yeast cells. The yeast promoters are induced by a fermentable carbon source such as glucose or a non-fermentable carbon source such as ethanol or both. Therefore expression of nucleic acid molecules encoding a polypeptide under the control of the novel yeast promoters are regulated by varying the level of a fermentable carbon source or a non-fermentable carbon source or both. The yeast promoters

New promoter sequences from Saccharomyces cerevisiae useful for controlling expression of homologous and heterologous nucleic ac expression in yeast cells.

acid

Claim 1; Page 67-68; 191pp; English.

WPI;

2001-367697/38.

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RESULT 2
AAD07497
ID AAD0
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AC AAD0
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DT 10-A
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DE PYMR
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Best Local S
Matches 723
       PYMR251AP DNA plasmid
                           10-AUG-2001
                                                               AAD07497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are useful for, inter alia, the high level production of proteins or polypeptides in yeast cell culture. The present DNA sequence is Saccharomyces cerevisiae YMR25IWA promoter related to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 723 BP; 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                              standard;
                                                                                                                                                            GGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTAGAACAGGGGCTACA
                                                                                                                               CAT 723
                                                                                                                                                   TCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCTTAACTTT
                                                                                                                                                                                                  TCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTTCTGGGACGTCTTAACTTT
                                                                                                                                                                                                                           TTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGGGAGTTGTTTTCAA
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                                                                                                             CAT 723
                                                                                                                                                                                                                                          TTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGGGAGTTGTTTTTCAA
                                                                                                                                                                                                                                                                                 TGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCGGAGAACATAGTGATAAGGGATGTAAC
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                           (first entry)
                                                               DNA;
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                                                               11427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 723; DB 4;
Pred. No. 9.2e-211;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 723;
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Best Local Similarity
Matches 723; Conserv
                                                                                                                                                                                                                                                                                          Sequence 11427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-NOV-1999;
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                                                                                                                                                                                                                                                                                                            YMR251WA promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified.
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New promoter sequences from Saccharomyces cerevisiae useful for controlling expression of homologous and heterologous nucleic acid expression in yeast cells.

Example 4; Page 133-143; 191pp; English.

The invention relates to yeast promoters that are used to control the expression of homologous and heterologous muclaic acids encoding proteins and polypeptides in yeast cells. The yeast promoters are induced by a fermentable carbon source such as glucose or a non-fermentable carbon source such as glucose or a non-fermentable carbon source such as ethanol or both. Therefore expression of nucleic acid molecules encoding a polypeptide under the control of the novel yeast promoters are regulated by varying the level of a fermentable carbon source or a non-fermentable carbon source or both. The yeast promoters are useful for, inter alia, the high level production of proteins or polypeptides in yeast cell culture. The present sequence is pYMRZ51AP plasmid related to the invention. This plasmid contains pPRB1 and yeast YMRZ51WA promoter

Qy	1 CTTTCGATTAGCACGCACACACACATAGACTGCGTCATAAAAATACACTACGGAAAA 60	
₽	15 CTTTCGATTAGCACGCACACACATCACATAGACTGCGTCATAAAAATACACTACGGAAAA 74	
Qy	61 ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAAGGAGCACGCTTGTAAGGGGGAT 120	
ᅡ	75 ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGGAT 134	
Qy	121 GGGGCTAAGAAGTCATTCACTTTCTCTTTTCCCTTCGCGGTCCGGACCCCGGGACCCCTCCT 180	
Db	135 GGGGGCTAAGAAGTCATTCACTTTCTTTTCCCTTCGCGGTCCGGGACCCCGGGACCCCTCCT 194	
Qy	181 CTCCCCGCACGATTTCTTTCTTCATATCTTTCTTTATTCCTATCCCGTTGAAGCAACC 240	
ф	195 CTCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATCCCGTTGAAGCAACC 254	
Qy	241 GCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTG	
В	255 GCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTATCTCACAGT 314	
Qy	301 GGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTAGAACAGGGGCTACA 360	
Db	315 GGTAACGGCACCGTGGCTCGGAAAACGGTTCCTTCGTGACAATTCTAGAACAGGGGCTACA 374	
γo	361 GTCTCGATAATAGAATAAGCGCATTTTTGCTAGCGCCGCGCGCG	

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The invention relates to yeast promoters that are used to control the expression of homologous and heterologous nucleic acids encoding proteins and polypeptides in yeast cells. The yeast promoters are induced by a fermentable carbon source such as glucose or a non-fermentable carbon source such as glucose or a non-fermentable carbon molecules encoding a polypeptide under the control of the novel yeast promoters are regulated by varying the level of a fermentable carbon source or a non-fermentable carbon source or both. The yeast promoters
                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae Unidentified.
                                                                                                                                                                                                                                                                                                         Yeast; promoter; gene expression; fermentable carbon source; glucose; non-fermentable carbon source; ethanol; yeast cell culture; pyMRZ51AP plasmid; luciferase gene; ds.
                                                                                                   New promoter sequences from Saccharon controlling expression of homologous expression in yeast cells.
                                                                                                                                                                                                                                                                                                                                             pYMR251AP+luc sequence
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                                                                                   Example
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                                                                                                                                                                                                                17-NOV-2000; 2000WO-SE002277
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                                                                                  3; Page 88-99; 191pp; English.
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heterologous nucleic ad
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Best Local Similarity
Matches 723; Conserv
            10-AUG-2001
                                              AAD07503
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                             AAD07503;
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                                               standard;
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                                                                                             738
            (first
                                               DNA;
            entry)
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                                               850
                                               ВP
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are useful for, inter alia, the high level production of proteins or polypeptides in yeast cell culture. The present sequence is pYMR251AP+luc sequence DNA construct related to the invention. The pYMR251AP+luc sequence contains pPRB1 plasmid, luc backbone (luciferase gene) and yeast YMR251WA promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTAGAACAGGGGCTACA
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                     TCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCTTAACTTT
                                                                                                 TCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCTTAACTTT
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Pred. No. 3.5e-210;
; Mismatches 0;
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Yeast

YMR251WA promoter region

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                                                                                                                                                                                                           The invention relates to yeast promoters that are used to control the expression of homologous and heterologous nucleic acids encoding proteins and polypeptides in yeast cells. The yeast promoters are induced by a fermentable carbon source such as glucose or a non-fermentable carbon source such as glucose or a non-fermentable carbon molecules encoding a polypeptide under the control of the novel yeast promoters are regulated by varying the level of a fermentable carbon source or a non-fermentable carbon source or both. The yeast promoters are useful for, inter alia, the high level production of proteins or polypeptides in yeast cell culture. The present DNA sequence is saccharomyces cerevisiae YMR251WA promoter region related to the
                                                                                                                                                                                                                                                                                                                                                                                       New promoter sequences from Saccharomyces cerevisiae useful for controlling expression of homologous and heterologous nucleic acid expression in yeast cells.
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09-JAN-2001;
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                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 680 BP; 180 A; 142 C; 166 G; 192 T; 0 U; 0 Other;
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AAAAAGACTAATAATAACA 722
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Pred. No. 1.3e-141;
0; Mismatches 1;
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Best Local S
Matches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chang H,
Katagiri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      illustrate the invention.
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                                                                                                                                                                       TCTTCCTTTCATATCTTCCTTTATTCCTATCCCGTTGAAGCAACCGCACTATGACTAAA
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  WRMWRMTRRRWAKKSSRTSRRKKRKWCMRKRKYKRMRGYSRMRSCKRARWMKRCRSGRA
                                                     TGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTATCTCACAGTGGTAACGGCACCGT
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F, Quan
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S, Tao Y,
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(ie Z, Zhu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bursitis; cirrhosis; hepatitis; polycythaemia vera; anaemia; psoriasis; primary thrombocytopenia; cancer; adenocarcinoma; leukaemia; myeloma; sarcoma; immune system disorder; acquired immunodeficiency syndrome; AIDS; allergy; asthma; Crohn's disease; diabetes mellitus; gout;
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; 2001US-0262208P.

2001US-0262599P.

2001US-0262599P.

2001US-0262760P.

2001US-0263063P.

2001US-0263066P.

2001US-0263070P.

2001US-0263074P.

2001US-0263077P.

2001US-0263077P.

2001US-0263077P.

2001US-0263329P.
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2001US-0261979P.
2001US-0261981P.
2001US-0262164P.
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Matches Query Match

80;

Conservative

<u>.</u>.

Mismatches

69;

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Gaps

0

Local

Similarity

5.3%;

Score 38.6; DB 6; Pred. No. 0.94;

Length Indels

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CC expression of functional SPTM, e.g. actinic keratosis, arteriosclerosis, CC bursitis, cirrhosis, hepatitis, polycythaemia vera, primary thrombocytopenia, anaemia, psoriasis, cancers including adenocarcinoma, CC leukaemia, myeloma or sarcoma, immune system disorder such as acquired cimmunodeficiency syndrome (AIDS), allergies, asthma, Crohn's disease, CC diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout, CC Hashimoto's thyroiditis, hepatitis, multiple sclerosis, osteoporosis, CC pancreatitis, Reiter's syndrome, autoimune thyroiditis or rheumatoid CC arthritis, neurological disorders such as epilepsy, stroke, Alzheimer's CC disease, pick's disease, Huntington's disease, dementia, Parkinson's CC disease, other developmental disorder of the central nervous system, CC mental disorder including mood, anxiety or schizophrenic disorder, manesia or Tourette's disorder. The polynucleotides may be used in CC hybridisation and amplification technologies, e.g. in assessing gene CC expression patterns, to develop a transcript image for a particular cell or tissue, or to create transgenic animals to model human disease. This cCC sequence encodes a human secretory protein isolated in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes an isolated polynucleotide a naturally occurring polynucleotide sequence at least 90 % identical to it, a polynucleotide complementary to it or an RNA equivalent of it. The purified secretory polypeptides (SPTM) and polynucleotides are useful in the diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New purified secretory polypeptides and polynucleotides, useful in the diagnosis, study, prevention or treatment of diseases associated with decreased expression of functional secretory molecules, e.g. AIDS, cancer
Sequence 2311 BP; 824 A; 325 C; 473 G; 689 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 260-261; 340pp; English.
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is B, Flores V,
Peralta CH, Da
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V, Daffo A,
David MH, I
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                                                                                                                                                                                                            RESULT
               Colon cancer; T cell; tumour protein; C6348; C6358; C6378; C6408; humoral immune response; cellular immune response; cytostatic; immunostimulant; human; ss.
                                                                                                              16-DEC-2004
                                                                                                                                            ADT96256;
                                                                                                                                                                          ADT96256 standard; cDNA; 544
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                                                                              cancer
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                                                                             associated human cDNA sequence #1763.
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DNA organisation;

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                                                                                                                                                                                                                                                                                                                                                    The invention relates to polynucleotide and polypeptide sequences CC associated with cancer, particularly colon cancer. Also disclosed are (i) CC an expression vector comprising the polynucleotide, (ii) a host cell CC transformed or transfected with the expression vector, (iii) an isolated antibody, or its antigen-binding fragment, which specifically binds to CC the polypeptide, (iv) a method of detecting or determining the presence CC of cancer in a patient, (v) a fusion protein comprising at least one of the polypeptides, (vi) an oligonucleotide that hybridises to the polypeptide sequence under highly stringent conditions, and (vii) a CC method of stimulating and/or expanding T cells specific for a tumour CC protein. The polypeptide specifically comprises the amino acid sequence of C344S, C635S, C637S, C640S, C636S or one of the potential open reading CC frames (ORFS) of C636S. These polypeptides are encoded by the CC polynucleotide sequences, where both are capable of eliciting a humoral CC and/or cellular immune response. The polynucleotides, polypeptides, and CC antibodies are useful for diagnosing, preventing or treating cancer. CC particularly colon cancer. The polynucleotide and polypeptide sequences are also useful in DNA strand invasion, antilense inhibition, mutational CC analysis, nucleic acid purification, isolation of transcriptionally antilense, blocking or transcription factor binding, genome cleavage, CC of insttu hybridisation, and as enhancer of transcription or color associated colons. Note: The sequence represents a human colon cancer associated CC cDNA. Note: The sequence data for this patent was obtained in electronic colors at directly from the USPTO web site at sequata. uspto.gov
                                                                                RESULT
                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 69
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07-FEB-2001; 2001US-0267382P.
11-MAY-2001; 2001US-0290322P.
12-JUL-2001; 2001US-0305265P.
16-AUG-2001; 2001US-0313077P.
                 AAS29224;
                                                                                                                                                                                                                                                                                                                              Sequence 544 BP; 181 A; 70 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acids and polypeptides capable of eliciting humoral and/or cellular immune response, useful for diagnosing, preventing or treating cancer, particularly colon cancer.
                                              AAS29224 standard; DNA; 7736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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ilarity 57.5%;
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Smith CL,
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; Pred. No. 0.55
0; Mismatches
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L, Durham M,
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14-AUG-2000;
14-AUG-2000;
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14-JUL-2000;
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19-MAY-2000;
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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;

Human nervous system related polynucleotide SEQ ID NO

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                                  TTGAAGCAACCGCACTA
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                                                                                            GGACCCCTCTCTCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cid molecules encoding human secreted chromosomal binding used in preventing, treating or ameliorating a disorder, 's and Parkinson's diseases and cancers.
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PR 13-OCT-2000; 2000US-0239375P PR 20-OCT-2000; 2000US-0239375P PR 20-OCT-2000; 2000US-02417865P PR 20-OCT-2000; 2000US-02417865P PR 20-OCT-2000; 2000US-02417865P PR 20-OCT-2000; 2000US-02418266P PR 20-OCT-2000; 2000US-02446175P PR 20-OCT-2000; 2000US-02446523P PR 20-OCT-2000; 2000US-0246525P PR 20-OCT-2000; 2000US-0246527P PR 20-OCT-2000; 2000US-0246527P PR 20-OCT-2000; 2000US-0246610P PR 20-OCT-2000; 2000US-0246610P PR 20-OCT-2000; 2000US-0246613P PR 20-OCT-2000; 2000US-0246613P PR 20-OCT-2000; 2000US-0249212P PR 20-OCT-2000; 2000US-024921P PR 20-OCT-2000; 2	21-SEP-2000; 2000US-0234; 21-SEP-2000; 2000US-0234; 25-SEP-2000; 2000US-0234; 25-SEP-2000; 2000US-0235; 26-SEP-2000; 2000US-0235; 27-SEP-2000; 2000US-0235; 29-SEP-2000; 2000US-0236; 02-OCT-2000; 2000US-0237, 02-OCT-2000; 2000US-0237, 02-OCT-2000; 2000US-0237,

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hyperproliferative disorder; cancer; renal disorder; arrhythmia; acute glomerulonephritis; cardiovascular disorder; respiratory diso Goodpasture's syndrome; neurological disorder; Alzheimer's disease; Parkinson's disease; endocrine disorder; Addison's disease; reproductive system disorder; endometriosis; infectious disease; viral infection; bacterial infection; fungal infection; vaccine;
                                                                                                                                                                                                                                   Human; DNA-binding protein; B cell immunodeficiency; autoimmune disorder; severe combined immunodeficiency; rheumatoid arthritis; Crohn's disease; diabetes mellitus; allergy; asthma; inflammatory condition; thrombosis;
                                                                                                                                                                                                      diabetes mellitus; allergy; asthma; inflammatory condition; thrombograft-versus-host disease; blood-related disorder; atherosclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME
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                                                                                                                                                                                                                                                                                                                                                                                                 14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
      Novel DNA-binding protein useful for diagnosis, prognosis, prevention treatment of immune, hyperproliferative, respiratory, cardiovascular, reproductive, endocrine, gastrointestinal and neurological disorders.
                                                                       (ROSE/)
(RUBE/)
(BARA/)
                                                                                                                08-DEC
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14-AUG-2000;
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                                        2002-690611/74.
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                                                                       ROSEN C A
RUBEN S M
BARASH S
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2000US-0235834P.
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RESULT 12
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ID ADC254
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Best Local
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                                                                                                                                                                                                                                                                                         Extracellular matrix protein; cytostatic; antibacterial; virucide; neuroprotective; gynaecological; gastrointestinal-Gen; cardiant; cardiovascular-Gen; nephrotropic; antiinflammatory; muscular-Gen; respiratory-Gen; immunosuppressive; cerebroprotective; vasotropic; nootropic; antiallergic; cancer; bacterial infection; viral infection; neural disorder; immune system disorder; blood disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gastrointestinal disorders (e.g. Crohn's disease). The invention is also useful to stimulate neuronal growth and treat, prevent, and/or diagnose neuronal damage which occurs in certain neuronal disorders or neuro-degenerative conditions. The present nucleic acid sequence represents a human DNA-binding protein genomic DNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                pulmonary did
inflammatory
                                                                                                                                                                                                                                                      muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA from extracellular matrix gene 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADC25486 standard; cDNA;
  31-JAN-2000; 2000US-0179065P
                                         07-MAR-2002; 2002US-00091483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC25486;
                                                                                                                              US2003049650-A1
                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                proliferative disorder;
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Pred. No. 2.9;
0; Mismatches
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02-MAR-2000;
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2000US-0234273P.
2000US-0234279P.
2000US-023499P.
2000US-0235484P.
2000US-0235834P.
2000US-0235834P.
2000US-023532P.
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2000US-0216880P.
2000US-0217487P.
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2000US-0218290P.
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2000US-0232401P.
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2000US-0231242P.
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2000US-0227182P.
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2000US-0225447P.
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  New DNA-binding treating and/or
                                                              2003-605749/57.
DB; ADC25241.
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2000US-0251988P
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proteins and gene encoding them, preventing e.g. neurological, in
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S-0251030P.
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em, useful for diagnosing, inflammatory, infectious,
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cc novel genes. Also included are recombinant vectors, host cells
convergence of the protein, the extracellular matrix proteins (including
their fragments, epitopes and homologues), an isolated antibody that
cc binds specifically to the protein, diagnosing a pathological condition or
susceptibility to a pathological condition (comprising determining the
cc presence or absence of a mutation in the nucleic acid and diagnosing a
cc condition based on the presence or absence of the mutation), diagnosing a
cc pathological condition or susceptibility to a pathological condition
cc (comprising determining the presence or amount of expression of the
cc protein in a biological sample and diagnosing a condition based on the
cc presence or amount of expression of the protein), preventing, treating or
cc ameliorating a medical condition by diministering the nucleic acid or
cc protein to a mammalian subject, identifying a binding partner to the
cc protein, the gene corresponding to the cDNA sequence, and identifying an
activity in a biological assay (comprising expressing the nucleic acid in
calculation the consensator determine the material abiological
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17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                              Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a cell, isolating the supernatant, detecting an activity in a biological assay and identifying the protein in the supernatant having the activity). The nucleic acids and proteins display the following activities Cytostatic, antibacterial, Virucide, Neuroprotective,
                                                                                                                                                        20-FEB-2001; 2001WO-US005171.
                                                                                                                                                                                                     23-AUG-2001
                                                                                                                                                                                                                                           WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                             Human prostate expression marker cDNA 4385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABV04394;
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; 2000US-0207454P.
; 2000US-0211314P.
; 2000US-0219007P.
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MILLENNIUM

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RESULT 14
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Best Local Sim:
Matches 56;
31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cancer has merastraized in a patient; (f) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a nucleotide sequence given in Tables 1-9 specification or its complement (T) a patient is affiliation.
                                                                                                                                                                                                                                                                                                                                    Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
                                                                                                                                                                                                                                                                                                                         musculoskeletal
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2000US-0179065P.
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17-NO
The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies
                                                                                                                       Claim
                                                                                                                                                   Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculcancers and also for testing and detection e.g. diagnosis.
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31-JAN-2000;
04-FEB-2000;
28-JUN-2000;
07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      periodontal regeneration; tissue transport; bone graft; skin aging; keratinocyte growth; hair loss; melanocyte growth; cell proliferation; cell growth; organ transplant; cell differentiation; body height; weight hair colour; sye colour; skin; percentage of adipose tissue; pigmentation; cosmetic surgery; metabolism; biorhythm; caricadic rhythm; depression; tendency for violence; pain; reproductive capability; hormone level; endocrine level; appetite; libido; memory; stress; storage capability; fat content; lipid content; protein content; carbohydrate content; vitamin content; cofactor content;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene; ss; musculoskeletal system antigen; cancer; metastasis; re-vascularisation; thrombosis; arteriosclerosis; mineral content; cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
                                                                                                                                                                                       17-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIDS-related complex; chondrocyte growth; bone regeneration;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene; ss; musculoskeletal system antigen; re-vascularisation; thrombosis; arterioscl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                        10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   post-operative tissue repair; limb regeneration; neuronal growth; neurodegenerative disorder; Alzheimer's disease; Parkinson's dise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                               sapiens
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; 2000US-0179065P.
; 2000US-0180628P.
; 2000US-0214886P.
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       The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, burns, post-operative tissue repair, and ulcers; stimulates angiogenesis and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcers; stimulates angiogenesis and limb regenerative tissue repair, and ulcers; stimulates and prevent neuronal damage occurring in certain disorders or neurodegenerative conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or
                                                                                                                                                                                                                                       Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer.
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14 - AUG-
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Best Local Similarity
Matches 88; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    keratinocyte growth; prevents hair loss, since FGF family members activate hair-forming cells and promotes melanocyte growth; stimulates growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines; maintains organs before transplantation or for supporting cell culture of primary tissues; induces tissue of mesodermal origin to differentiate in early embryos; increases or decreases the differentiation or proliferation of embryonic stem cells, besides, haematopoietic lineage; modulates mammalian
                                                                                                                                                                                                                                                                                                                                                        Sequence 366 BP; 120 A; 59 C; 53 G; 133 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                   printed specification, but wa
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                                                                                       GAAGGACCAGTGTTTCTTCTCTATGCTGCAACCAATTCCAAATGTTGGCTTTTTAGGTAA
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/cgn2_6/ptodata/1/pubpna/PCTUS_FUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

00	Result No.
723 723 723 720.4 497.4 497.4	Score
100.0 100.0 100.0 99.6 68.8 5.7 5.7	Query Match
100.0 723 100.0 11427 100.0 13073 99.6 850 68.8 680 5.7 1024 5.7 1024	Query Match Length DB ID
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US-10-776-213-2 US-10-776-213-24 US-10-776-213-20 US-10-776-213-30 US-10-776-213-30 US-10-451-467A-317 US-10-123-155-198 US-10-146-731-198	ID
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Sequence 2883, Ap	1976,	e 819,	319, A	9439	25183,	Sequence 25182, A	25183,	25182,	e 1068	1068	æ	106	965	e 436	e 333	333,	129	e 29	e 55	e 55:	e 27	e 27	e 177	e 23	e 13	Sequence 20, Appl	e 19	e 19	e 198,	e 198,	e 198,	e 198,					

## ALIGNMENTS

RESULT 1 US-10-776-213-2

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Sequence 2, Application US/10776213

Publication No. US20040142478A1

GENERAL INFORMATION:
APPLICANT: ASTERAGENECA AB

TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for Controlling Nucle
TITLE OF INVENTION: Acid Expression
FILE REFERENCE: 3526,82543

CURRENT APPLICATION NUMBER: US/10/776,213

CURRENT APPLICATION NUMBER: US/10/776,213

CURRENT FILING DATE: 2004-02-12

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 723

TYPE: DNA

ORGANISM: Saccharomyces cerevisiae

US-10-776-213-2
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                         ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGAT 120
                                                                                                                             CTTTCGATTAGCACGCACACACATCACATAGACTGCGTCATAAAAATACACTACGGAAAA 60
  ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGAT 120
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RESULT 2
US-10-776-213-24
; Sequence 24, Application US/10776213
; Publication No. US20040142478A1
; Publication No. US20040142478A1
; Publication No. US20040142478A1
; GENERAL INFORMATION:
GENERAL INFORMATION: Compositions and Methods Utilizing Sequences for Controlling Nucl
; TITLE OF INVENTION: Acid Expression
FILE REFERENCE: 3526,82543
; CURRENT APPLICATION NUMBER: US/10/776,213
; CURRENT FILING DATE: 2004-02-12
; NUMBER OF SEQ ID NOS: 32
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                                                                                                    ; LENGTH: 11427
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-776-213-24
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                                                       100.0%; Score 723; DB 19; ilarity 100.0%; Pred. No. 4.7e-216; Conservative 0; Mismatches 0;
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Sequence 20, Application US/10776213

Publication No. US20040142478A1

GENERAL INFORMATION:
APPLICANT: AstraZeneca AB

TITLE OF INVENTION: Compositions and Methods Utilizing Seq
TITLE OF INVENTION: Acid Expression
FILE REFERENCE: 3526.82543

CURRENT APPLICATION NUMBER: US/10/776,213

CURRENT FILING DATE: 2004-02-12

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 20
LENGTH: 13073
               Query Match
Best Local Similarity
Matches 723; Conserva
                                                                                                ; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-776-213-20
                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-10-776-213-20
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                             100.0%; Score 723; DB 19; ilarity 100.0%; Pred. No. 5.1e-216; Conservative 0; Mismatches 0;
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RESULT 4
US-10-776-213-30
| Sequence 30, Application US/10776213
| Publication No. US20040142478A1
| GENERAL INFORMATION:
| APPLICANT: AstraZeneca AB
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                              ; TYPE: DNA ; ORGANISM: Saccharomyces cerevisiae US-10-776-213-30
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                                                         TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for Controlling Nucl TITLE OF INVENTION: Acid Expression FILE REFERENCE: 3526.82543 CURRENT APPLICATION NUMBER: US/10/776,213 CURRENT FILING DATE: 2004-02-12 NUMBER OF SEQ ID NOS: 32 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 30 LENGTH: 850
Query Match
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; Sequence 317, Application US/10451467A
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; GENERAL INFORMATION:
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APPLICANT: CONTRERAS, ROLAND HENRI
APPLICANT: EBERHARDT, INES
APPLICANT: EBERHARDT, INES
APPLICANT: REEKMANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRU
TITLE OF INVENTION: YEAST AND FUNGI
FILE REFERENCE: JAB-1667
CURRENT APPLICATION NUMBER: US/10/451,467A
CURRENT FILING DATE: 2003-06-19
PRIOR APPLICATION NUMBER: EP 00870318.3
PRIOR APPLICATION NUMBER: EP 01870002.1
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-01-04
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RESULT 6
US-10-123-155-198/c
                                                                                                        GENERAL INFORMATION:
APPLICANT: Baker, Kevi
APPLICANT: Beresini;
APPLICANT: DeForge, I
APPLICANT: Desnoyers
APPLICANT: Filvaroff
APPLICANT: Gao, Wei-c,
APPLICANT: Gaodard, J
APPLICANT: Goddard, J
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                                                                                                                                                                                                                                    Sequence 198, Application US/10123155 Publication No. US20030068794A1
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PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 317
LENGTH: 680
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                                                                               Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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                                       Smith, Victoria
Stewart, Timothy A.
                                                                                                                                                  Desnoyers, Luc
Filvaroff, Ellen
Watanabe, Colin K
Wood, William
                           Tumas, Daniel
                                                                   Sherwood, Steven
                                                                                                                         Gerritsen, Mary E
                                                                                                                                       Gao, Wei-Qiang
                                                                                                                                                                               DeForge, Laura
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Pred. No. 1.2e-145;
0; Mismatches 1;
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RESULT 7 US-10-146-731-198/c

Sequence 198, Application US/10146731
Publication No. US20030129692A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen

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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333R1C30
CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
LENGTH: 1024
TYPE: PRT
ORGANISM: Homo Sapien
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Best Local
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DM.S.M.ATMR...H
                                                                .YBBBCSMAAA,YRA.NG.TWT.RRASK..A.S.DHABWCH...BSA.B.KNS.S.RAT.
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                               AAGACTAATAATAAC
                                                                                                GAGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGG 646
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SEQ ID NO 198
LENGTH: 1024
TYPE: PRT
ORGANISM: Homo Sapien
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                                                                   GAGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGG
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                                                                                                     ACB...RDT.C.M.WBH.WWB.AB.HC.W.DG..DB.BKABH..RS.SSBS.H...Y..B
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Desnoyers, Luc
Filvaroff, Ellen
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Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C168
CURRENT APPLICATION NUMBER: US/10/140,472
CURRENT FILING DATE: 2002-05-06
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
LENGTH: 1024
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Publication No. US20030138888A1
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Best Local Similarity
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APPLICANT:
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                        52; Conservative 194; Mismatches 429;
               GCGCCCGTTTCCCAATAGGGAGGCGCAGTTTATCGGCGGAGCTCTACTTCCTATTTG 466
                                                 SBDSYNCBB.A...W.RSNN..M.TMAMTS.HR..D..A...YN.TAANC..A.B.RCK 595
                                                                                                                                                                                 RN.KYH..MH..R.TYSTTDW...HM..S.RY.....N...RCTYT.S.THH..CTYNS
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                                                                                                                BS.B.DNY...H...YWNY.HRNBY.RCA.N.NC..WSCMH.RA.YDD.SMNSBW..T.S
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                                                                                                                                                                                                                   CCGTTGAAGCAACCGCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGT
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Wood, William
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Gerritsen, Mary E.
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Filvaroff, Ellen
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US-10-141-761-198
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US-10-141-761-198/c
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CURRENT APPLICATION NUMBER: US/10/141,761
CURRENT FILING DATE: 2002-05-08
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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ST. DGDMNC.SGT.K.B.YY...D.RST.B.SCN.NNM.WC.M.RAATB.M..R.N..N
                               CCGGGACCCCTCCTCCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATC 226
                                                                 GA.T...MM.SBTAASD.MKW...WBH.H..SBCAGRB.HYBN...YNYNSS.WHS..A 835
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Wood, William
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                    US-10-142-885-198
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NUMBER OF SEQ ID NOS:
SEQ ID NO 198
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/142,885
CURRENT FILING DATE: 2002-05-10
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                                    TYPE: PRT
ORGANISM: Homo
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Wood, William
Zhang, Zemin
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Stewart, Timothy
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Godowski, Paul J.
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Sequence 198, Application US/10158790
Publication No. US20030180879A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desorgers, Luc
APPLICANT: Desorgers, Luc
APPLICANT: Desorgers, Luc
APPLICANT: Genoyers, Luc
APPLICANT: Goo, Wei-Qiang
APPLICANT: Goodard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
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 Stewart, Timothy A. Tumas, Daniel
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RESULT 12 US-10-137-871-198/c

Sequence 198, Application US/10137871 Publication No. US20030207350A1 GENERAL INFORMATION:

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; APPLICANT: Zhang, Zemin
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POI
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C448
; CURRENT APPLICATION NUMBER: US/10/158,790
; CURRENT FILING DATE: 2002-05-30
; Prior Application removed - See File Wrapper or Paymener OF SEQ ID NOS: 550
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LENGTH: 1024
TYPE: PRT
ORGANISM: Homo
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93330R1C153
CURRENT APPLICATION NUMBER: US/10/137,871
CURRENT FILING DATE: 2002-05-03
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ACB...RDT.C.M.WBH.WWB.AB.HC.W.DG..DB.BKABH..RS.SSBS.H...Y..B
                                                                                                  ATAAGGGATGTAACTTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGG
                                                                                                                                 ..TTCMMRT.WH.BYH.HAT..B..SB.DSST.CH..KB.D.BHA..Y.M.KNWC.R.RH
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Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K
Wood, William
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DeForge, Laura
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RESULT 13
US-10-140-923-198/c
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NUMBER OF SEQ ID NOS: 550
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TYPE: PRT
ORGANISM: Homo S
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CURRENT FILING DATE: 2002-05-07
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TITLE OP INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OP INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C188
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SBDSYNCBB.A...W.RSNN..M.TMAMIS.HR..D..A...YN.TAANC..A.B.RCK
                                                            BS.B.DNY...H...YWNY.HRNBY.RCA.N.NC..WSCMH.RA.YDD.SMNSBW..T.S
                                                                                                                          RN.KYH..MH..R.TYSTTDW...HM..S.RY....N...RCTYT.S.THH..CTYNS
                                                                                                                                                                                          ST..DGDWNC.SGT.K.B.YY...D.RST.B.SCN.NNM.WC.M.RAATB.M..R.N..N
                              GAACAGGGGCTACAGTCTCGATAATAGAATAATAAGCGCATTTTTGCTAGCGCCGCCGCG
                                                                                          GTGTATCTCACAGTGGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTA 346
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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Wood, William
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Matches 52
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SEQ ID NO 198
LENGTH: 1024
TYPE: PRT
ORGANISM: Homo Sapien
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT FILING DATE: 2002-05-08
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Gurney, Austin L.
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774 RN.KYH..MH..R.TYSTTDW...HM..S.RY.....N...RCTYT.S.THH..CTYNS 715
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Prior Apploication removed - See File Wrapper or NUMBER OF SEQ ID NOS: 550 SEQ ID NO 198 LENGTH: 1024 TYPE: PRT GENERAL INFORMATION: Sequence 198, Application US/10141759 Publication No. US20030207361A1 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93330R1C197
CURRENT APPLICATION NUMBER: US/10/141,759
CURRENT FILING DATE: 2002-05-08 APPLICANT: Baker, Kevin P. ORGANISM: Homo Sapien Godowski, Paul J. Gurney, Austin L. Sherwood, Steven Gerritsen, Mary E. Goddard, Audrey Watanabe, Colin K Stewart, Timothy A Smith, Victoria Gao, Wei-Qiang Filvaroff, Ellen DeForge,Laura Beresini, Maureen Wood, William Tumas, Daniel Desnoyers, Luc

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294 DM.S.M.ATMR...H 280
                                                         354 YBBBCSMAAA YRA.NG.TWT.RRASK..A.S.DHABWCH...BSA.B.KNS.S.RAT. 295
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Search completed: August 27, 2005, 11:43:49 Job time: 658 secs

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Match
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1. /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4. /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6. /cgn2_6/ptodata/1/ina/backfIles1.seq:*
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							Query Mat Best Loca Matches	S-09-743-194-2 Sequence 2, A Patent No. 67 GENERAL INFOR APPLICANT: B APPLICANT: TITLE OF INV TITLE REFEREN CURRENT APPL CURRENT FILL RUMBER OF SE SOFTWARE: PA SEQ ID NO 2 LENGTH: 723 TYPE: DNA ORGANISM: S S-09-743-194-2		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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GTCTCGATAATAGAATAATAAGCGCATTTTTGCTAGCGCCGCCGCGCGGCGCCCGTTTCCCA	TAACGG	GCACTATGACTAAATGGTGCTGGACATCTCC	TCCCCGCAC		ACCATAAAGAGCAAAGCGATAC 	CTTTCGATTAGCACG	larit Conse	licat 601 TION: field field Filon: IION: 1352 ATION DATE ID NO ntin		**************************************
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APPLICANT: Oakley, Caroline
APPLICANT: Oakley, Caroline
TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for
TITLE OF INVENTION: Controlling Nucleic Acid Expression in Yeast
FILE REFERENCE: 3526.82543
CURRENT FILING DATE: US/09/743,194
CURRENT FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24.
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                                                           GCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTTGTGTGTATCTCACAGT
                                                                                                                                                                              GGGGGCTAAGAAGTCATTCACTTTCTTTTCCCTTCGCGGTCCGGACCCGGGACCCCTCCT 180
                                          GCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGTGTATCTCACAGT
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Pred. No. 9.8e-229;
0; Mismatches 0;
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; TYPE: DNA
; ORGANIEM: Saccharomyces cerevisiae
US-09-743-194-20
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US-09-743-194-20
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APPLICANT: Oakley, Caroline
TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for
TITLE OF INVENTION: Controlling Nucleic Acid Expression in Yeast
FILE REFERENCE: 3526.82543
CURRENT APPLICATION NUMBER: US/09/743,194
CURRENT APPLICATION NUMBER: US/09/743,194
CURRENT FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/09743194 Patent No. 6716601 GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                   ACCATAAAGAGCAAAGCGATACCTTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGGAT 120
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CTCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATCCCGTTGAAGCAACC
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APPLICANT: Oakley, Caroline
APPLICANT: Oakley, Caroline
TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for
TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for
TITLE OF INVENTION: Controlling Nucleic Acid Expression in Yeast
FILE REFERENCE: 3526.82543
CURRENT APPLICATION NUMBER: US/09/743,194
CURRENT FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
TYPE: DNA
COGRAISM: Saccharomyces cerevisiae
US-09-743-194-30
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Best Local Similarity 99.7
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30, Application US/09743194
Patent No. 6716601
GENERAL INFORMATION:
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                                                               GGGGGCTAAGAAGTCATTCACTTTCTCTTTCCCTTCGCGGTCCGGACCCCGGGACCCCTCCT
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  CTCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTATTCCTATCCCGTTGAAGCAACC
                                                                                                      ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGAT
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                                             GGGGGCTAAGAAGTCATTCACTTTCCCTTCGCGGTCCGGACCCGGGACCCCTCCT
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Pred. No. 1.5e-228;
0; Mismatches 1;
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Patent No. 5670367
GENERAL INFORMATION:
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                          APPLICANT: DORNER, F.
APPLICANT: SCHBIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & L
                                                                                                                                                                                                                                              CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                       STREET:
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US-09-949-016-17445
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                                                                                                    CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                   SOFTWARE: FastSEQ for Windows Version SEQ ID NO 17445
                                                                                                                                                                                                                                                                                                                                                                     Sequence 17445, Ap
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity Matches 11; Conserv
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                                                                                                                                                                                                                                                                            FILE REFERENCE: CL001307
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INFORMATION FOR SEQ ID NO:
                 ORGANISM: Human
                                  LENGTH: 4989
TYPE: DNA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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TYPE: nucleic acid
STRANDEDNESS: single
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Pred. No. 0.00024;
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768

ASSOCIATED
OF DETECTION AND USES THEREOF

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                                   RESULT 8
US-09-949-016-16850/c
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; ORGANISM: Human
US-09-949-016-17442
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PRIOR FILING DATE: 2000-10-20
PRIOR PPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Best Local S
Matches 75
Sequence 16850, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17442
LENGTH: 11440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                         8713 GAAGTACTCCACTCTCCCGAGTCTGCCTTTCCCTCATGGCCTCTGACCTCGCTCCCC 8654
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                                                                                                                                                   TTGAAGCAACCGCACTA 246
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54.7%;
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0; Mismatches
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS:

207012

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SEQ ID NO 16850
LENCTH: 16662
TYPE: DNA
                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: 44 Human Secreted Proteins FILE REFERENCE: PZ024P1 CURRENT APPLICATION NUMBER: US/09/369,247 CURRENT FILING DATE: 1999-08-05 EARLIER APPLICATION NUMBER: 60/074,118 EARLIER FILING DATE: 1998-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 60/074,341
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/074,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 60/074,157
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/074,137
EARLIER FILING DATE: 1998-02-09
                                                                                                                                                                                                                                                                                                                                                                                      EARLIER FILING DATE: 1998-02-09
NUMBER OF SEQ ID NOS: 172
                                                                                                                                                                                                                                       NAME/KEY: SITE LOCATION: (406) OTHER INFORMATION:
                                                                                                                                                                       NAME/KEY: SITE
LOCATION: (794)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                          ENGTH: 815
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Local Similarity 54.0%;
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                                                              594 TTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCT
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TCCCTTCGCGGTCCGGACCCGGGACCCTCCTCCCCGCACGATTTCTTCCTTTCATAT 208
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                               TATCCTGTTATTTAAATGTGAACATTTATTGTACATTCAGTGAGTTATAGTGTTAATAGT
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                                                                                            Score 35.8; DB Pred. No. 0.34; 0; Mismatches
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Pred. No. 1.1;
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US-09-949-016-16144
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                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION UNMERE: US/09/949,016

CURRENT APPLICATION AND DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 16144
LENGTH: 191433
                                                                                                                                                     SEQ ID NO 15419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6812339
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
NAME/KEY: misc_feature
LOCATION: (1)...(212449)
OTHER INFORMATION: n = A,T,C
                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
                                                               ORGANISM: Human FEATURE:
                                                                                                                               LENGTH: 212449
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o. 6812339
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Pred. No. 12;
0; Mismatches
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OF DETECTION AND USES THEREOF
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RESULT 13
US-09-949-016-14133/c
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                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTIC
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
SOFTWARE: Fast
SEQ ID NO 14133
                                                                                                                                                                                                                                                                                                  Sequence 14133, Application US/09949016
Patent No. 6812339
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                                 PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FAPPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR EPLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,498
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                 FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTICTICCTTICATATCTTCCTTTATTCCTATCC 227
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Pred. No. 13
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/247,768
PRIOR FILLING DATE: 2000-10-03
PRIOR FILLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILLING DATE: 2000-09-08
PRIOR FILLING DATE: 2000-09-08
VUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17100
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                                                                                                                                                                                                                                                                                                                  LENGTH: 102884
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(102884)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17100,
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ORGANISM: Human
FEATURE:
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LOCATION: (1)...(98962)
OTHER INFORMATION: n = A,T,C
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1 Similarity 53.7%;
72; Conservation
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                                     CATATCTTCCTTTT 217
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TTTTTTTTTTTT 78392
                                                                                                             TCTTTTCCCTTCGCGGTCCGGACCCCGGGACCCCTCCTCCCCGCACGATTTCTTCCTTT
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Pred. No. 13;
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Pred. No. 13;
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RESULT

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Sequence 26160, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

TYPE: DNA

ORGANISM: Human

US-09-949-016-26160
Search completed: August 27, 2005, 10:04:45 Job time : 182 secs
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                                                                                              289 CATT 286
                                                                                                                                                 145 CTTT 148
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                 GenEmbl: *
1: 9b bas: *
2: 9b has: *
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Copyright (c) 1993 - 2005 Compugen Ltd.
SUMMARIES
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AL161797	AX664151	AC106212	AC150010	AC150295	AC026346	AC102413	AC016156	AC104663	AC006434	AC117108_0	AC136942	AC146425	AC091952	CR382131_37	AX655393	AC113236	AC099664	AC110665	PFMAL3P7	AC111758	AC009868	AC009649	AC090639	AL157889
AL161797 F	AX664151 S	AC106212 F	AC150010 C	AC150295 C	AC026346 H	AC102413 Mus	AC016156 H	AC104663 H	AC006434 C		AC136942 H	AC146425 F	AC091952 H	Continuation (38 o	AX655393 S	AC113236 C	AC099664 F	AC110665 C	AL034559 E	AC111758 F	AC009868 F	AC009649 F	AC090639 H	
Human DNA	Sequence	Rattus no	Callithri	Callithri	Ното варі	Mus muscu	Homo sapi	Homo sapi	Genomic s	Rattus no	Ното варі	Pan trogl	Ното варі	ion (38 o	Sequence	Canis fam	Homo sapi	Canis fam	Plasmodiu	Rattus no	Homo sapi	Ното варі	Ното варі	Human DNA

## ALIGNMENTS

Qy 241 GCACTATGACTAAATGGTGCTGGACATCT	Qy 181 CTCCCCGCACGATTTCTTCCTTTCATATCT	Qy 121 GGGGGCTAAGAAGTCATTCACTTTCTTTTV	Qy 61 ACCATAAAGAGCAAAGCGATACCTACTTG	Qy 1 CTTTCGATTAGCACGCACACACACACAT.	Query Match 100.0%; Score 723; Best Local Similarity 100.0%; Pred. No. 3. Matches 723; Conservative 0; Mismatches	SOURCE Unknown.  SOURCE Unknown.  ORGANISM Unknown.  Unclassified. 723)  REFERENCE 1 (bases 1 to 723)  AUTHORS Belfield,G.P. and Oakley,C.  TITLE Compositions and methods utilizing County of the Cou	ARA92027 LOCUS DEFINITION Sequence 2 from patent US 6716601 ACCESSION ARA92027 VERSION ARA92027 ARA92027 ARA92027.1 GI:47260496
GCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTG	CTCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTATTCCTATCCCGTTGAAGCAACC 240	GGGGGCTAAGAAGTCATTCACTTTCTTTTCCCTTCGCGGTCCGGACCCGGGACCCCTCCT 180	ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGAT 120	CTTTCGATTAGCACGCACACACATCACATAGACTGCGTCATAAAAATACACTACGGAAAA 60	Score 723; DB 6; Length 723; Pred. No. 3.8e-207; Mismatches 0; Indels 0; Gaps 0;	ng the yeast ZEO1 promoter	DNA linear PAT 15-MAY-2004

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Belfield,G.P. and Oakley,C.
Compositions and methods utilizing the
Patent: US 6716601-A 24 06-APR-2004;
Location/Qualifiers
                                                                                                                                                                                                                                                                                              Unknown.
Unclassified.
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Similarity 100.0%;
23; Conservative 0;
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                                              GGGGGCTAAGAAGTCATTCACTTTCTTTTCCCCTTCGCGGTCCCGGACCCCGCGCCCTCCT
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CTCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTATTCCTATCCCGTTGAAGCAACC
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Sequence 20
AR492045
AR492045.1
                                                                                                                                                                                                   1 (bases 1 to 13073)
Belfield,G.P. and Oakley,C.
Compositions and methods utilizing to Patent: US 6716601-A 20 06-APR-2004;
Location/Qualifiers
                                                                                                                                                                                                                                                        Unclassified
                                                                                                                                                                                                                                                                   Unknown
                                                                                                                                                                                                                                                                            Unknown.
                                                                                                                             Similarity
GGGGGCTAAGAAGTCATTCACTTTCCTTTCCCGTCGGGTCCGGGACCCGGGACCCCTCCT
                                              ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAAGGAGCACGCTTGTAAGGGGGGAT
                                                                         CAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                           TCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCTTAACTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTCGATGAGAGAATTAGCAAGCGGAAAAAAAACTATGGCTAGCTGGGAGTTGTTTTTCAA
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                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      723
                                                                                                                                                                                           1. .13073
                                                                                                                                                                       /organism="unknown"
/mol_type="genomic
                                                                                                                                                                                                                                                                                                  GI:47260514
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                                                                                                                                                                    _type="genomic
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                                                                                                                  Score 723; DB 6;
Pred. No. 6.3e-207;
Mismatches 0;
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US 6716601
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Q b Q	Query N Best Lo Matcher	AUTHORS TITLE JOURNAL FEATURES SOURCE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 4 AR492055 LOCUS DEFINITION	Db Qy	g &	gg Qy	B &	gg Qy	DB 69	B 8	B 8	D Qy	D Qy	ф
1 CTTTCGATTAGCACGACACACATCACATAGACTGCGTCATAAAATACACTACGGAAAA 60	/ Match 99.6%; Score 720.4; DB 6; Length 850; Local Similarity 99.9%; Pred. No. 2.4e-206; Lee 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	S Belfield,G.P. and Oakley,C. Compositions and methods utilizing the yeast ZEO1 promoter L Patent: US 6716601-A 30 06-APR-2004; Location/Qualifiers rce			721 CAT 723     736 CAT 738	661 TATTGCAGAGGACTATCAAATCATACAGATATTGTCAAAAAAAA	601 TCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCTTAACTTT 660	541 TTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGGGAGTTGTTTTTCAA 600	481 TGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCGGAGAACATAGTGATAAGGGATGTAAC 540	421 ATAGGGAGGCGCAGTTTATCGGCGGAGCTCTACTTCTTCCTATTTGGGTAAGCCCCCTTTC 480	361 GTCTCGATAATAGAATAATAAGCGCATTTTTGCTAGCGCCGCCGCGGCGGCCGCCGTTTCCCA 420	301 GGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTAGAACAGGGGCTACA 360 	241 GCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTATCTCACAGT 300	181 CTCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATCCCGTTGAAGCAACC 240	136 GGGGGCTAAGAAGTCATTCACTTTCTTTTCCCTTCGCGGTCCGGAACCCGGGACCCCTCCT 195
COMMENT	TITLE JOURNAL	SOURCE ORGANISM ORGANISM REFERENCE AUTHORS JOURNAL REFERENCE	RESULT 5 SC9920 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	Db Qy	Qy e	Qy e	Qy S	Qy 4	Qy Db	Qу 3	Qу 3 ДЪ 3	Qy 2	Qy I	Qy 1	Db 1
CB10 1RQ E-mail: barrell@sanger.ac.uk Notes: Notes: All CDS over 100 codons have been analysed. CDS that are completel overlapped and those that are overlapped by more than 50% of their length by a larger CDS have been omitted from this analysis.	Barrell, B., Rajandream, M.A. and Walsh, S.V.  Barrell, B., Rajandream, M.A. and Walsh, S.V.  Direct Submission  Submitted (10-MAR-1995) Saccharomyces cerevisiae chromosome XIII  sequencing project, Sanger Centre, Hinxton Hall, Hinxton, Cambridg	PETIII; transfer RNA-Ala, Saccharomyces cerevisiae (baker's yeast) SM Saccharomyces cerevisiae Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.  E 1 (bases 1 to 23498) S Hunt,S. and Bowman,S. Unpublished E 2 (bases 1 to 23498)	SC9920 S.cerevisiae chromosome XIII cosmid 9920. 248639 Z71257 Z48639.1 GI:732924 COX7: cytochrome oxidase: delta element: dlutamate decarboxylase:	721 CA 722   798 AA 799	661 TATTGCAGAGGACTATCAAATCATACAGATATTGTCAAAAAAAA	601 TCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCTTAACTTT 660	541 TTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGGGAGTTGTTTTTCAA 600	481 TGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCGGAGAACATAGTGATAAGGGATGTAAC 540	421 ATAGGGAGGCGCAGTTTATCGGCGGAGCTCTACTTCCTATTTGGGTAAGCCCCTTTC 480	361 GTCTCGATAATAGAATAAGCGCATTTTTGCTAGCGCCGCGCGCG	301 GGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTAGAACAGGGGCTACA 360	241 GCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTG	181 CTCCCCGCACGATTTCTTCCTTTCATATCTTTCTTTATTCCTATCCCGTTGAAGCAACC 240	121 GGGGCTAAGAAGTCATTCACTTTCTTTTCCCTTCGCGGTCCGGACCCCGGGACCCCTCCT 180	138 ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGAT 197

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and at the
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Cosmid 9920 is overlapped at the start of this sequence by cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSARNSAEVLNEFWTNFLKFAEDSSEERVKKMVESEIFNSLSCGKSLSEYTKLNQTLS
GVFPPDKWEREIEDYFTSDEDIRKIKVSFEKNLFALLVTSPNNESAISRLFDFFVQLI
ETDPSNVFNKYDGVYDALNYFLDSDMIFLNGKIGKFINEIPTLVQESTYQNFAGIMAQ
                      complement (4197.
                                                                                                                                                                                         small spliced gene"
                                                                                                                                                                                                                                 complement (join (4101.
/note="YM9920.03c, unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="tRNA-Ala, anticodon complement(3379. .3706)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(2406. .2438)
/note="PS00061 Short-chain alcohol dehydrogenase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVLLNSIDTVSSTTLNGLLASVESFVTKTVRDQKSTDKDYLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TDDKFINLKNMQKLIRYALFLDALLDALPERVNNHIVAFITVVSELVTDYNCLSEEPN
DLYYDFGHTFFKHGKVNLNFSDIVGNVIQPANGGDAMLTFDIAESNSVYFFYYSRVLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YSNIKFFKANTDAITSLEDFFIVALSFNLPKTIILATMNELDNDIYQQLMKSDSLELE
LYIEDFMKNYKEDDSGEIFKGNIKFLKQFITTTLYSAVANGQVEQFCAVLSKLDETF
FSTILLLHTDFLSCALYEVSEDTNIKFLKGFLGLAKGNSEIANKLAQVILQHAQYYFSB
GAKEKYVTHAVELINGCNDTSQIFFPANAIEVFARYMPAIDYRSSLVSSLSTNTHLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="msfggintfqqyntdlglghngvrislnyfdglpdpsllnslys
NELKLIfKSLLKRDETTKEKALMDLSNLISDFNQNEYFFNDIFLLCWSQIYAKLIISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="YM9920.01c, unknown, PS00061 Short-chain alcohol
                                                 ALAHLCAIYTE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="YM9920.02c, unknown, small spliced gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (join (4101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="tRNA-Ala"
/note="tPNA-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKEKVLKFLSVSRTSPSPGFFNAVFALYSSTKRHSFLDYYLEWLPFWQKSVQRLNEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MPSHKNIMKLAVKKLLKSLTHITSKNILKVCPVLPSILNLLATLDDYEDGTIWSYDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDPAKINALMAVFQEQLLNI,VKEIVVNENEDTISDERYSSKEESEFRYHRVIASAVLL
LIKLFVHNKDVSERNSSSLKVILSDESIWKLLNLKNGQNTNAYETVLRLIDVLYTRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YKVIRLQSHQITIMLVKSLRKKISKFLKDFIPLILLGTCELDYSVSKPSLNELTECFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAA88574.1"
/db_xref="GI:732925"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 signature"
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                                                                                                               /protein_id="CAA88576.1"
/db_xref="GI:732927"
                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAA88575.1"
/db_xref="GI:732926"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e end of this sequence by Location/Qualifiers
                                                                                                                                                              product="unknown"
                                                                                                                                                                                                                                                                                        [PLNSLALAHLCAIYTE"
                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="delta element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="UniProt/Swiss-Prot:Q04781"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="cosmid 9920"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="AB972"
                                                                     translation="MELMASCFRMPRYRHANDTLGWLLIGHRRLLPLNNKAIIPLNSL
                                                                                              db_xref="UniProt/TrEMBL:Q8X1Y9"
                                                                                                                                                                                                                                                                                                              translation="MGELAPMNKPDEGITNMCQSLYRYQIMRMSIGLRRLLPLNNKAI"
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                                                                                                                                                                                                                                                                                                                                    _xref="UniProt/TrEMBL:Q8X1Z0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _xref="taxon:4932"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type="genomic DNA"
splice acceptor sequence,
                        .4199)
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dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAI: 0.17, possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 "
                                                                                                                                                                                                                                        CAI: 0.13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAI:
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/note="YM9920.06c, unknow
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VYKAGFAECAEVYEREVTSLFQYLDKLENLLDKKYTDLEAEYGKNNKDKI LDRYFA I G
DTLTEADVRLYPTI VRFDVVYHQHFKCNLATI RDDYSR I HTWLKNI YWRHEAFQRTTD
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pcpwaQrtlitralkglapiigcsvahwhLddkgwrfLeegdgktnerhwfdiaggis
svnLntstpvanipnnahrLLvDgtdephygykrLsdpyfkTkpdykgrftvpvLwdL
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KKFHEEYPEVPQAILSSLLRGRGWIIFNYPLPKATDGSDEKEVLRVVFRSEMKLDLAQ
LLIVDIESILTKLIHSYEKVCHHIELASEQTPERKSSFIYEMLLALASPQDDIPTPDE
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LDPESIWDYVDENTIGGFVILGTTYTGHLENVEKVADVLSQIEAKHPDWSNYDIPIHA
DGASGGFIIPGFEKEHMKAYGMERWGFNHERVVSNNTTSGHKFGLTTPGLGWYLWRDE
SLLADELRFKLKYLGGVEETFGLNFSRPGFQVVHQYFNFVSLGHSGYRTQFONSLFVA
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snnmrdtssogmankysvpkkglpadlsyolihneltldgnphlnlasfvntfttdoa
rklidenltknladndeypolieltorcismlaolmhanpdeepigcattgsseaiml
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/note="possible donor squence,
complement(4689..4694)
                          YYSLMYLTISDAVLITFLAPSLTIFLSWVILRERFTKVEALGSLISLLGVVLIVRPSF
LFGTPELTDSSSQIVESSDPKSRLIATLVGLWGVLGMSCVYIIIRYIGKRAHALMSVS
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Nedenvdgnettlqriskdylkpniglvlltvsyffnsamvvstkvlendpdblandr
                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (10777. .12021)
/note="YM9920.07c, unknown,
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/note="YM9920.05, unknown, len: 366, CAI: 0.11, similar t
YK56_YEAST P36156, YKR076W, hypothetical protein in SIS2,
                                                                                                QIKPLQILLVRMVITYIGTLIYMYINKSTISDVPFGKPEVRKWLVLRGCTGFFGVFGM
                                                                                                                                                                                       /db_xref="GOA:Q04835"
/db_xref="SGD:S0004866"
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/db_xref="GI:732931"
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/protein_id="CAA88578.1"
/db_xref="G1:732929"
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complement(4428. .4433)
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/FSLITAIVSFIGINTIPSMKFQIPHSKKQWILFGNLGVSGFIFQLLLTMGIQRERAG
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translation="MFGKVFVSYIRTRIGFKPLSTIYTPVSSSSLSFDKEACFPFKKW
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db_xref="UniProt/Swiss-Prot:Q04792"
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/db_xref="GI:732928"
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TTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGGGAGTTGTTTTTCAA
                                                           TGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCGGAGAACATAGTGATAAGGGATGTAAC
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                                        TGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCGGAGAACATAGTGATAAGGGATGTAAC
                                                                                          ATAGGGAGGCGCAGTTTATCGGCGGAGCTCTACTTCTTCCTATTTGGGTAAGCCCCCTTTC
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/note="YM9920.08c, unknown,
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coiled-coil domain"
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DVTYTMHVFYMTIILILVRKQMQSIHAFLGSLCLPSHVLDFSIVRDILSWYFLETVAV
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TPIIDDEENSIPLTEFDLSDSK"
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/db_xref="GI:732932"
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Pred. No. 4.2e-206;
0; Mismatches 1;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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AX536716
AX536716.1 GI:25263152
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TGGGACGTCTTAACTTTATTGCAGAGGACTATCAAATCATACAGATATTGTCAAAAAAA
                                                                              TGGGAGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTC
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                                                          TGGGAGTTGTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTC
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PHARMACEUTICA N.V. (BE)
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/mol_type="unassigned DNA"
/db_xref="taxon:4932"
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1 (bases 1 to Gardner, M.J.,
              Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
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Plasmodium falciparum
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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14 from patent US 5670367.
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Hall, N., Fung, E.,
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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/locus tag="PF11 0071"
complement(<2647...>4074)
/locus tag="PF11 0071"
complement(2647...4074)
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ASVLNSYLRPKKTEITEKLRVEINKTVNKFLESGLABIIFGVLYIDBAHMADIECTSV
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ILALRAQTEKINITEEGMNYLAKIGIQSSLRFAMLLLEPSRILATLEGNTIIDIKHIE
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vvprlygkhlfvekroffstlyfvttllmkdvtkihavlvayerrksleffvlgikk
anivilvnkkpkkimepniksisfsitavinskmdetipstkvtlflfisilstkiv"
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complement(join(<14)4.
/locus_tag="PF11_0070"
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/db_xref="GI:23495997"
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'chromosome="11"
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25280 CGAGAGAACTATAATGTACGAGATGAAAAGGTATAATAATGACA 2532:
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                                                                                                                                                                                                                                                                                                                                                                                                         AGCGGAAAAAACTATGGCTAGCTGGGAGTTGTTTTCAATCATATAAAAGGGAGAAATT
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12185. .12400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46.8; DB 3; Pred. No. 0.04;
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VRT 06-JAN-2004

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                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived length of mononuclectide A/T runs and conserved TA repeats. Where this is found the mononuclectide A/T runs and conserved TA repeats.
                                                                                                                                                                   648
                                                                                                                                                                                                                                                                                                                                    78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Materman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-144B6 is from a CHORI-11 BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-JAN-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jan 6, 2004 this sequence version replaced gi:37805672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Danio rerio (zebrafish)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Wellcome Trust Sanger Institute Center code: SC
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/clone="CH211-144B6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Danio rerio"
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57.8%;
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Pred. No. 0.3;
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Homo sapiens BAC clone RP11-107
AC092573 AC015764
AC092573.2 GI:15668nov
                                                                                                                           Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6: On Sep 19, 2001 this sequence version replaced gi:14916158
                                                                                                                                                                                                    Waterston,R.
Direct Submission
                                                                                                                                                                                                                                                                                            Submitted (19-SEP-2001) Genome
                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                4 (bases 1 to 171265) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                     Submitted (19-JUL-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boyer, E. The sequence of Homo sapiens BAC clone RP11-107
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Sulston, J.E. and Waterston, R.
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                                                                                                                                                                                                                                                                            University School of
                                                                                                                                                                                                                                                                                                                                                                      MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center project name: H_NH0001007
Drafting Center: WIBR
                                                                      Center: Washington University Genome Sequencing Center Center code: WUGSC Web site: http://genome.wustl.edu/gsc
                                                     Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cotton, M.,
                                Summary Statistics
                                                                                                                                                                                                                                                                            Medicine,
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                                                                                                                                                                                                                                                                            Sequencing Center, Washington 4444 Forest Park Parkway, St.
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from 2,
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                                                                                                                                                                  63108,
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between neighboring data submissions. clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap This sequence may not represent the entire insert of this

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence restriction digest. from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise noted:

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information of Genetics, Washington University, St. Louis
MC. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

## SOURCE INFORMATION:

The RPCI-11 human BAC library was made donor, as described by Osoegawa, K., Woo Woon, P.Y., Zhao, B., F Frengen, E.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either Research Genetics, Inc. (http://www.resgen.com) or Pieter de and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Data from AC013461, AC073465, AC011667 finish this clone, AC015764.
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/note="match to EST BE867724
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}588. .3651
                                                  note="match to EST
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                                                                                                                                                                                                                                                                                     note="match to EST AL537636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="similar to Homo sapiens EST AL524174 NNID:912787667)"
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(mol_type="genomic DNA"
(db_xref="taxon:9606"
                                                                                 note="match to EST
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. .2351
                                                                                                                                                _family="CR1"
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                                                                                                                                                                                 _family="Alu"
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                                                BE867724 (NID:g10316500)
                                                                                   AW814670
                                                                                                                 AL537636
                                                                                                                                                                                                                                                                                   (NID:g12801129)
                                                                                (NID: 97907664) "
                                                                                                                 (NID:g12801129)"
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                                                                                                                                                                                                                                                                                                                    (NID:g10316500)"
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                             GCTATAAAAAGGAGAAATTAATCCACACAATCTCACACATTCTGGGAGGAAAAATAAACT
                                                                                       CATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGGACGTCTTA-ACTTT
                                                                                                                                  TTTAGTAAAAAAAAAAAAAAAAAAAAAATGCTGGGTTTGTTACTCTCGTTTTTGACA 56049
 TTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGGGAGTTGTTTTTCAAT
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(NID:g10153317)"
                                                                                                                                                                                                                                                                                                                  (NID: 98624596) "
                                                                                                                                                                                                                                                                                                                                    note="similar to Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       note="match
                                                                                                                                                                                                                                                                                                                                                                                                      'note="match to EST AI347484
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                                                                                                                                                                                                 Score 43.6; DB Pred. No. 0.34; O; Mismatches
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REFERENCE
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55928 CA
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B lirren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,

B lirren, B., Linton, L., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,

Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Conelan, L., Doyle, M.,

FitzHugh, W., Forrest, C., Funke, R., Gage, D.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Galagan, J., Cardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,

McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,

Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,

Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
                                          Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-primer-amersham; 3% of reads
Chemistry: Dye-terminator Big Dye; 97% of reads
Chemistry: Dye-terminator Big Dye; 97% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 191830 bases at least Q40
Consensus quality: 19935 bases at least Q30
Consensus quality: 203385 bases at least Q30
Insert size: 210000; agarose-fp
Insert size: 206529; sum-of-contigs
Quality coverage: 4.0 in Q20 bases; agarose-fp
Quality coverage: 4.1 in Q20 bas.
* NOTE: This is a "working draft' sequence. It currently
consists of 23 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robearch, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 21, 2000 this sequence version replaced gi:7321517.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 208729)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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208729 bp DNA linear Homo sapiens chromosome 2 clone RP11-337F19 map 2, SEQUENCE, 23 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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               as soon as it is available and the be preserved.
                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1385
Center clone name: 337_F_19
                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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1080: contig of 1080 bp in length
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2, clone RP11-337F19
                                   accession number
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WORKING DRAFT
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                                                   /note="assembly_fragment"
12712. .14921
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                 note="assembly_fragment"
                                                                                                  'note="assembly_fragment'
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152522: gap of
178409: contig :
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208729: contig o
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f 100 bp
g of 5662 bp in length
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f 100 bp
g of 23447 bp
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of 8105 bp in length
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Muzny, D., Arenson, A.D., Adams, C., Brundage, E., Bunac, C., Carvelli, K., Chacko, J., Chen, J., Di, W., Ding, Y., Dugan, S., Durbin, J., Forcum, J., Ganesh, R., Garcia, C., Goodman, M., Gorrell, J.H., Haywood, M., Hernandez, J., Jackson, L., Jin, S., Kampal, R., Karpathy, S., Kovar, C., Leal, B., Li, Y., Lichtarge, O., Liu, W., Logan, O., Lu, J., Ly, T., Martinez, C., Oswal, G., Perez, L. Rashid, N.D., Rowland, K., Savage, L., Scherer, S.E., Shen, H.,
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Direct Submission
Submitted (11-APR-1998) Molecular and Human Genetics, Baylor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (17-SEP-1998) Human Genome Sequencing Center, Depar
of Molecular and Human Genetics, Baylor College of Medicine,
Baylor Plaza, Houston, TX 77030, USA
(bases 1 to 80659)
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Adrian Smit.
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
                                                                                                                                                                                                                                                                                                    note="overlaps bases 114570.
                                                                                                                                                                                                                                                                                                                                        clone="GSHB-223P11"
                                                                                                                                                                                                                                                                             function="clone overlap"
                                                                                                                                            _family="Aluy"
._20%^
                                                                                                                                                                                                                                                                                                                                                                               _xref="taxon:9606"
                                                                                                                                                                                                                                        _family="L2"
        family="MER5B
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Genetics, Baylor College
TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes were chosen if there maintained sequence continuity
                                                                                                                                                                                                                                                                                                      .116568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Powerblast by Jinghui
                                                                                                                                                                                                                                                                                                      of clone AC112492"
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of Medicine, One
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repeat\_region

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\_family="MER5A"

\_family="MER3" family="(CA)n"

repeat\_region repeat\_region

/rpt

family="L1MC4" ement (10600

complement (9246. .9302)
/rpt family="AT\_rich"
complement (9663. .10244

family="MIR" \_family="AT\_rich"

complement (11161...11220)
/rpt\_family="(GA)n"
complement (12725...12846)

complement (10630. .10701)
/rpt\_family="(TA)n"

/rpt\_family="(TA)n"
complement(12853. ...

ement (12853. .12932) family="(CATA)n"

/rpt\_

family="MIR"

3428

repeat\_region repeat\_region repeat\_region

repeat\_region

complement(6228. .6290)
/rpt family="MLT1D"
complement(6354. .6624)

complement (6631.

family="L1MA2"
ement(6621)

t family="MLT1D" plement(7635..7690)

repeat\_region repeat\_region

complement (5319 ...5358)
/rpt family="AT rich"
complement (5853 ...5898)
/rpt family="AT rich"
complement (5943 ...6244)
/rpt family="MUTIE"
/rpt family="MUTIE"

repeat\_region

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REFERENCE
AUTHORS
TITLE
                                                                               KEYWORDS
SOURCE
ORGANISM
                                                                                                                                   ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                 33266 AACATGCTAAGAGATTAACTTAAGTGTTAATTTTAAGGGAATAACTTGAGCGTTCTGTGC 33207
                                                                       N Homo sapiens chromosome X clone RE SEQUENCE, 9 unordered pieces. 1 AC021710.4 GI:7408016 HTG; HTGS PHASE1; HTGS DRAFT. Homo sapiens (human) 4 Homo sapiens
                                                                                                                                                                                                                                                                                                                  697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        577 GGCTAGCTGGGAGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGA 636
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 195932)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome X, clone RP11-12D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.9%;
Similarity 51.0%;
                                                                                                                                                                                                                                                                                   ATGAAAAAAAAAAAAA 33129
                                                                                                                                                                                                                                                                                                                                                                               CAGTTTCTGGGACGTCTTAACTTTTATTGCAGAGGACTATCAAATCATACAGATATTGTC 696
                                                                                                                                                                                                                                                                                                                  AAAAAAAAAAAAGACTAA 714
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(35042...35071)
/rpt_family="AT_rich"
complement(35418...35439)
/rpt_family="AT_rich"
complement(38090...38123)
/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (33176. .33223)
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(32126. .32237)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(30273...31278)
/rpt_family="MER11A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /standard_name="G19948"
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29361. .29554
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complement(28749. .29386)
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/rpt_family="L2"
complement(28709..28748)
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. .26997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family="AluSx"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42.8; DB Pred. No. 0.52; 0; Mismatches
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                                                                                                                                                                                 DNA linear HTG 04-APR-2000 RP11-12D5 map X, WORKING DRAFT
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repeat\_region repeat\_region

complement (24998. .25210) /rpt family="L1PA8" 25211. .25359

repeat\_region repeat\_region

'ada'

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/rpt\_family="AluSp"
complement(22905. ...
/rpt\_family="MIR"

.22958)

21804.

/rpt\_family="MER4A2"
21247. .21510

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family="MER4A"

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/rpt\_family="AT\_rich"

/rpt\_family="MLT1C" 18083. .1813/

complement (16745. .17110) /rpt\_family="L1M4"

ıdı,

family="L2"

/rpt\_family="AT\_rich"
complement(14686. .14)

family="FLAM\_C"
. 15925

ď 'zgt

family="L1PA8" 14188

.14150)

complement (18177

family="MADE1"

family="L1MA9"
. 190cc

/rpt\_t 20350.

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JOURNAL
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                           FEATURES
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source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Roderson, S., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Cheepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Crant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McCheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, G., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., M., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Almer, A. and Zodv, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 4, 2000 this sequence version replaced gi:6939568.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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2 (basea 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrasp; version 0.960731
Consensus quality: 189137 bases at least Q40
Consensus quality: 19288 bases at least Q30
Consensus quality: 19288 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 195132; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 5.0 in Q20 bases; Quality coverage: 4.9 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
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49251
73383
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                           Location
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104624: contig
104724: gap of
142393: contig

    Genome Center

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of 53439 bp in length.
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of 16370 bp
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of 13086 bp in length
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of 24132 bp
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of 9021 bp in length
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189032 AACATGCTAAGAGATTAACTTAAGTGTTAATTTTAAGGGAATAACTTGAGCGTTCTGTGC 189091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   517 GAACATAGTGATAAGGGATGTAACTTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTAT 576
requests: clonerequest@sanger.ac.uk
On Mar 12, 2001 this sequence version replaced gi:13092292.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                  complete sequence.
AL359542
                                                                    Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgesh CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 28858)
                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                         Human DNA sequence from clone
                                                                                                          Direct Submission
                                                                                                                                                                                                                                                     AL359542.13
                                                                                                                            Heath, P.
                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                          AL359542
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/db_xref="taxon:9606"
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RP6-190D15 on chromosome Xq25-26.1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMPORTANT: This sequence is not the entire insert of clone RP6-190D15 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP4-537K23 is at 28759 in this sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Group. Further information can
http://www.sanger.ac.uk/HGP/ChrX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The true left end of clone RP4-537K23 is at 28759 in this sequence. The true right end of clone RP4-753P9 is at 100 in this sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          database can be found at
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                                                                                                                                                                                                                                                                                                10287. .10362
/note="38 copi
10380. .10462
/note="L1MB3 r
                                                                                                                                                                                                                                            10464. .10518
/note="7SK repeat: matches 1.
                                                                                                            note="AluSg repeat: matches 24.
|2081. .12122
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                                                         .2927.
                                                                             note="AluSg repeat: matches 253. .294 of consensus"
                                                                                                                                                                  .1889. .12080
                                                                                                                                                                                      note="AluSx repeat:
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note="L2 repeat: matches 2602.
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mol_type="genomic DNA"

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24 copies 2 mer
.13842
                                                                                                                                                                                                                                                                                                                                                            copies 2 mer aa 69% conserved"
                                                                                                                                                                                                                                                                                                   repeat: matches 6035. .6127 of consensus"
                                                                                                                                                                                         matches 1.
                      gt 72% conserved"
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                                                                                                                                      .296 of consensus"
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                                                                                                                                                           25970
                               note="AluSc repeat: matches 1, .306 of consensus"
                                                                                                      note="AluSx repeat: matches 1. .312 of consensus"
                                                                                                                                    note="49 copies 2 mer ag 61% conserved"
                                                                                                                                                                          'note="AluSx repeat: matches 1.
                                                                                                                                                                                                           note="LIME repeat: matches 5500. .5714 of consensus"
                                                                                                                                                                                                                                                                                                              note="L1M4 repeat: matches 5627. .5818 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                       note="MIR repeat: matches 115.
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/note="L1MA9 repeat: matches 6110. .6218 of consensus"
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/note="L1MA2 repeat: matches 6213.
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/note="L1M4_r
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                                                                     note="MER51B
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                                                                                                                                                                                                                                                                                                                                                   note="AluSx repeat: matches 1. .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                        note="U6 repeat: matches 1. .30 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L1PA8 repeat: matches 5489. .6163 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="AluSg repeat: 0699. .21369
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note="TIGGER2 repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ote="Weakly double-stranded"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e="L1MB4 repeat: matches 5646. .6176
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                                                                                                                                                                                                                                                                                      During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at the primary accession the wormper tables and the part of the second of the se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13671 AC 13670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      590 TTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (26-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestes clonerequest@sanger.ac.uk Cone revenuestes clonerequest@sanger.ac.uk On Jul 29, 2002 this sequence version replaced gi:21727348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL645468 209764 bp DNA linear ROD 26-JUL-2002 Mouse DNA sequence from clone RP23-246F18 on chromosome 4, complete
                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-246F18 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 209764)
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                                                                   Location/Qualifiers
/organism="Mus musculus"
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                                                                                                                187 GCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATCC 227
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                                                         TICCCCTTTCCCTTTCCCTTTTCCTTTCCTTTCC
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                      /clone="RP23-246F18"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/db_xref="taxon:10090"
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